

OIIPE

## RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/928,175

TIME: 11:21:34

Input Set : A:\001229seq.txt

Output Set: N:\CRF3\08162001\I928175.raw

3 <110> APPLICANT: Paszty, Christopher J.  
 4 Gong, Jianhua  
 5 Daugherty, Betsy  
 6 Rogers, Norma  
 8 <120> TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and  
 9 Uses Thereof  
 11 <130> FILE REFERENCE: 00-1229  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/928,175  
 C--> 14 <141> CURRENT FILING DATE: 2001-08-10  
 16 <150> PRIOR APPLICATION NUMBER: 60/224,455  
 17 <151> PRIOR FILING DATE: 2000-08-10  
 19 <160> NUMBER OF SEQ ID NOS: 42  
 21 <170> SOFTWARE: PatentIn Ver. 2.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2265  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
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 30 <222> LOCATION: (1)..(2262)  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: sig\_peptide  
 34 <222> LOCATION: (1)..(108)  
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 38 Met Ile Val Phe Leu Val Phe Lys His Leu Phe Ser Leu Arg Leu Ile  
 39 1 5 10 15  
 41 aca atg ttc ttt cta ctt cat ttc atc gtt ctg atc aat gtc aaa gat 96  
 42 Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp  
 43 20 25 30  
 45 ttt gca ctg act caa ggt agc atg atc act cct tca tgc caa aaa gga 144  
 46 Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly  
 47 35 40 45  
 49 tat ttt ccc tgt ggg aat ctt acc aag tgc tta ccc cga gct ttt cac 192  
 50 Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His  
 51 50 55 60  
 53 tgt gat ggc aag gat gac tgt ggg aac ggg gcg gac gaa gag aac tgt 240  
 54 Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys  
 55 65 70 75 80  
 57 ggt gac act agt gga tgg gcg acc ata ttt ggc aca gtg cat gga aat 288  
 58 Gly Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn  
 59 85 90 95  
 61 gct aac agc gtg gcc tta aca cag gag tgc ttt cta aaa cag tat cca 336  
 62 Ala Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro  
 63 100 105 110  
 65 caa tgc tgt gac tgc aaa gaa act gaa ttg gaa tgt gta aat ggt gac 384  
 66 Gln Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp

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67	115	120	125	
69	tta aag tct gtg ccg atg att tct aac aat gtg aca tta ctg tct ctt	432		
70	Leu Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu			
71	130	135	140	
73	aag aaa aac aaa atc cac agt ctt cca gat aaa gtt ttc atc aaa tac	480		
74	Lys Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr			
75	145	150	155	160
77	aca aaa ctt aaa aag ata ttt ctt cag cat aat tgc att aga cac ata	528		
78	Thr Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile			
79	165	170	175	
81	tcc agg aaa gca ttt ttt gga tta tgt aat ctg caa ata tta tat ctc	576		
82	Ser Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu			
83	180	185	190	
85	aac cac aac tgc atc aca acc ctc aga cct gga ata ttc aaa gac tta	624		
86	Asn His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu			
87	195	200	205	
89	cat cag cta act tgg cta att cta gat gac aat cca ata acc aga att	672		
90	His Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile			
91	210	215	220	
93	tca cag cgc ttg ttt acg gga tta aat tcc ttg ttt ttc ctg tct atg	720		
94	Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met			
95	225	230	235	240
97	gtt aat aac tac tta gaa gct ctt ccc aag cag atg tgt gcc caa atg	768		
98	Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met			
99	245	250	255	
101	cct caa ctc aac tgg gtg gat ttg gaa ggc aat aga ata aag tat ctc	816		
102	Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu			
103	260	265	270	
105	aca aat tct acg ttt ctg tcg tgc gat tcg ctc aca gtg ctg ttt ctg	864		
106	Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu			
107	275	280	285	
109	cct aga aat caa att ggt ttt gtt cca gag aag aca ttt tct tca tta	912		
110	Pro Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu			
111	290	295	300	
113	aaa aat tta gga gaa ctg gat ctg tct agc aat acg ata acg gag cta	960		
114	Lys Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu			
115	305	310	315	320
117	tca cct cac ctt ttt aaa gac ttg aag ctt cta caa aag ctg aac ctg	1008		
118	Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu			
119	325	330	335	
121	tca tcc aat cct ctt atg tat ctt cac aag aac cag ttt gaa agt ctt	1056		
122	Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu			
123	340	345	350	
125	aaa caa ctt cag tct cta gac ctg gaa agg ata gag att cca aat ata	1104		
126	Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile			
127	355	360	365	
129	aac aca cga atg ttt caa ccc atg aag aat ctt tct cac att tat ttc	1152		
130	Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe			
131	370	375	380	

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133	aaa	aac	ttt	cga	tac	tgc	tcc	tat	gct	ccc	cat	gtc	cga	ata	tgt	atg	1200
134	Lys	Asn	Phe	Arg	Tyr	Cys	Ser	Tyr	Ala	Pro	His	Val	Arg	Ile	Cys	Met	
135	385					390				395						400	
137	ccc	ttg	acg	gac	ggc	att	tct	tca	ttt	gag	gac	ctc	ttg	gct	aac	aat	1248
138	Pro	Leu	Thr	Asp	Gly	Ile	Ser	Ser	Phe	Glu	Asp	Leu	Leu	Ala	Asn	Asn	
139					405					410					415		
141	atc	ctc	aga	ata	ttt	gtc	tgg	gtt	ata	gct	ttc	att	acc	tgc	ttt	gga	1296
142	Ile	Leu	Arg	Ile	Phe	Val	Trp	Val	Ile	Ala	Phe	Ile	Thr	Cys	Phe	Gly	
143					420					425					430		
145	aat	ctt	ttt	gtc	att	ggc	atg	aga	tct	ttc	att	aaa	gct	gaa	aat	aca	1344
146	Asn	Leu	Phe	Val	Ile	Gly	Met	Arg	Ser	Phe	Ile	Lys	Ala	Glu	Asn	Thr	
147					435					440					445		
149	act	cac	gct	atg	tcc	atc	aaa	atc	ctt	tgt	tgt	gct	gat	tgc	ctg	atg	1392
150	Thr	His	Ala	Met	Ser	Ile	Lys	Ile	Leu	Cys	Cys	Ala	Asp	Cys	Leu	Met	
151					450					455					460		
153	ggt	ggt	tac	ttg	ttc	ttt	ggt	ggc	att	ttc	gat	ata	aaa	tac	cga	ggg	1440
154	Gly	Val	Tyr	Leu	Phe	Phe	Val	Gly	Ile	Phe	Asp	Ile	Lys	Tyr	Arg	Gly	
155	465					470					475					480	
157	cag	tat	cag	aag	tat	gcc	ttg	ctg	tgg	atg	gag	agc	gtg	cag	tgc	cgc	1488
158	Gln	Tyr	Gln	Lys	Tyr	Ala	Leu	Leu	Trp	Met	Glu	Ser	Val	Gln	Cys	Arg	
159					485					490					495		
161	ctc	atg	ggg	ttc	ctg	gcc	atg	ctg	tcc	acc	gaa	gtc	tct	gtt	ctg	cta	1536
162	Leu	Met	Gly	Phe	Leu	Ala	Met	Leu	Ser	Thr	Glu	Val	Ser	Val	Leu	Leu	
163					500					505					510		
165	ctg	acc	tac	ttg	act	ttg	gag	aag	ttc	ctg	gtc	att	gtc	ttc	ccc	ttc	1584
166	Leu	Thr	Tyr	Leu	Thr	Leu	Glu	Lys	Phe	Leu	Val	Ile	Val	Phe	Pro	Phe	
167					515					520					525		
169	agt	aac	att	cga	cct	gga	aaa	cgg	cag	acc	tca	gtc	atc	ctc	att	tgc	1632
170	Ser	Asn	Ile	Arg	Pro	Gly	Lys	Arg	Gln	Thr	Ser	Val	Ile	Leu	Ile	Cys	
171					530					535					540		
173	atc	tgg	atg	gcg	gga	ttt	tta	ata	gct	gta	att	cca	ttt	tgg	aat	aag	1680
174	Ile	Trp	Met	Ala	Gly	Phe	Leu	Ile	Ala	Val	Ile	Pro	Phe	Trp	Asn	Lys	
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177	gat	tat	ttt	gga	aac	ttt	tat	ggg	aaa	aat	gga	gta	tgt	ttc	cca	ctt	1728
178	Asp	Tyr	Phe	Gly	Asn	Phe	Tyr	Gly	Lys	Asn	Gly	Val	Cys	Phe	Pro	Leu	
179					565					570					575		
181	tat	tat	gac	caa	aca	gaa	gat	att	gga	agc	aaa	ggg	tat	tct	ctt	gga	1776
182	Tyr	Tyr	Asp	Gln	Thr	Glu	Asp	Ile	Gly	Ser	Lys	Gly	Tyr	Ser	Leu	Gly	
183					580					585					590		
185	att	ttc	cta	ggt	gtg	aac	ttg	ctg	gct	ttt	ctc	atc	att	gtg	ttt	tcc	1824
186	Ile	Phe	Leu	Gly	Val	Asn	Leu	Leu	Ala	Phe	Leu	Ile	Ile	Val	Phe	Ser	
187					595					600					605		
189	tat	att	act	atg	ttc	tgt	tcc	att	caa	aaa	acc	gcc	ttg	cag	acc	aca	1872
190	Tyr	Ile	Thr	Met	Phe	Cys	Ser	Ile	Gln	Lys	Thr	Ala	Leu	Gln	Thr	Thr	
191					610					615					620		
193	gaa	gta	agg	aat	tgt	ttt	gga	aga	gag	gtg	gct	gtt	gca	aat	cgt	ttc	1920
194	Glu	Val	Arg	Asn	Cys	Phe	Gly	Arg	Glu	Val	Ala	Val	Ala	Asn	Arg	Phe	
195	625					630				635					640		
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198 Phe Phe Ile Val Phe Ser Asp Ala Ile Cys Trp Ile Pro Val Phe Val
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201 gtt aaa atc ctt tcc ctc ttc cgg gtg gaa ata cca gac aca atg act 2016
202 Val Lys Ile Leu Ser Leu Phe Arg Val Glu Ile Pro Asp Thr Met Thr
203          660          665          670
205 tcc tgg ata gtg att ttt ttc ctt cca gtt aac agt gct ttg aat cca 2064
206 Ser Trp Ile Val Ile Phe Phe Leu Pro Val Asn Ser Ala Leu Asn Pro
207          675          680          685
209 atc ctc tat act ctc aca acc aac ttt ttt aag gac aag ttg aaa cag 2112
210 Ile Leu Tyr Thr Leu Thr Thr Asn Phe Phe Lys Asp Lys Leu Lys Gln
211          690          695          700
213 ctg ctg cac aaa cat cag agg aaa tca att ttc aaa att aaa aaa aaa 2160
214 Leu Leu His Lys His Gln Arg Lys Ser Ile Phe Lys Ile Lys Lys Lys
215 705          710          715          720
217 agt tta tct aca tcc att gtg tgg ata gag gac tcc tct tcc ctg aaa 2208
218 Ser Leu Ser Thr Ser Ile Val Trp Ile Glu Asp Ser Ser Ser Leu Lys
219          725          730          735
221 ctt ggg gtt ttg aac aaa ata aca ctt gga gac agt ata atg aaa cca 2256
222 Leu Gly Val Leu Asn Lys Ile Thr Leu Gly Asp Ser Ile Met Lys Pro
223          740          745          750
225 gtt tcc tag 2265
226 Val Ser
229 <210> SEQ ID NO: 2
230 <211> LENGTH: 754
231 <212> TYPE: PRT
232 <213> ORGANISM: Homo sapiens
234 <400> SEQUENCE: 2
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238 Thr Met Phe Phe Leu Leu His Phe Ile Val Leu Ile Asn Val Lys Asp
239 20 25 30
241 Phe Ala Leu Thr Gln Gly Ser Met Ile Thr Pro Ser Cys Gln Lys Gly
242 35 40 45
244 Tyr Phe Pro Cys Gly Asn Leu Thr Lys Cys Leu Pro Arg Ala Phe His
245 50 55 60
247 Cys Asp Gly Lys Asp Asp Cys Gly Asn Gly Ala Asp Glu Glu Asn Cys
248 65 70 75 80
250 Gly Asp Thr Ser Gly Trp Ala Thr Ile Phe Gly Thr Val His Gly Asn
251 85 90 95
253 Ala Asn Ser Val Ala Leu Thr Gln Glu Cys Phe Leu Lys Gln Tyr Pro
254 100 105 110
256 Gln Cys Cys Asp Cys Lys Glu Thr Glu Leu Glu Cys Val Asn Gly Asp
257 115 120 125
259 Leu Lys Ser Val Pro Met Ile Ser Asn Asn Val Thr Leu Leu Ser Leu
260 130 135 140
262 Lys Lys Asn Lys Ile His Ser Leu Pro Asp Lys Val Phe Ile Lys Tyr
263 145 150 155 160
265 Thr Lys Leu Lys Lys Ile Phe Leu Gln His Asn Cys Ile Arg His Ile
266 165 170 175

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268 Ser Arg Lys Ala Phe Phe Gly Leu Cys Asn Leu Gln Ile Leu Tyr Leu
269      180      185      190
271 Asn His Asn Cys Ile Thr Thr Leu Arg Pro Gly Ile Phe Lys Asp Leu
272      195      200      205
274 His Gln Leu Thr Trp Leu Ile Leu Asp Asp Asn Pro Ile Thr Arg Ile
275      210      215      220
277 Ser Gln Arg Leu Phe Thr Gly Leu Asn Ser Leu Phe Phe Leu Ser Met
278 225      230      235      240
280 Val Asn Asn Tyr Leu Glu Ala Leu Pro Lys Gln Met Cys Ala Gln Met
281      245      250      255
283 Pro Gln Leu Asn Trp Val Asp Leu Glu Gly Asn Arg Ile Lys Tyr Leu
284      260      265      270
286 Thr Asn Ser Thr Phe Leu Ser Cys Asp Ser Leu Thr Val Leu Phe Leu
287      275      280      285
289 Pro Arg Asn Gln Ile Gly Phe Val Pro Glu Lys Thr Phe Ser Ser Leu
290      290      295      300
292 Lys Asn Leu Gly Glu Leu Asp Leu Ser Ser Asn Thr Ile Thr Glu Leu
293 305      310      315      320
295 Ser Pro His Leu Phe Lys Asp Leu Lys Leu Leu Gln Lys Leu Asn Leu
296      325      330      335
298 Ser Ser Asn Pro Leu Met Tyr Leu His Lys Asn Gln Phe Glu Ser Leu
299      340      345      350
301 Lys Gln Leu Gln Ser Leu Asp Leu Glu Arg Ile Glu Ile Pro Asn Ile
302      355      360      365
304 Asn Thr Arg Met Phe Gln Pro Met Lys Asn Leu Ser His Ile Tyr Phe
305      370      375      380
307 Lys Asn Phe Arg Tyr Cys Ser Tyr Ala Pro His Val Arg Ile Cys Met
308 385      390      395      400
310 Pro Leu Thr Asp Gly Ile Ser Ser Phe Glu Asp Leu Leu Ala Asn Asn
311      405      410      415
313 Ile Leu Arg Ile Phe Val Trp Val Ile Ala Phe Ile Thr Cys Phe Gly
314      420      425      430
316 Asn Leu Phe Val Ile Gly Met Arg Ser Phe Ile Lys Ala Glu Asn Thr
317      435      440      445
319 Thr His Ala Met Ser Ile Lys Ile Leu Cys Cys Ala Asp Cys Leu Met
320      450      455      460
322 Gly Val Tyr Leu Phe Phe Val Gly Ile Phe Asp Ile Lys Tyr Arg Gly
323 465      470      475      480
325 Gln Tyr Gln Lys Tyr Ala Leu Leu Trp Met Glu Ser Val Gln Cys Arg
326      485      490      495
328 Leu Met Gly Phe Leu Ala Met Leu Ser Thr Glu Val Ser Val Leu Leu
329      500      505      510
331 Leu Thr Tyr Leu Thr Leu Glu Lys Phe Leu Val Ile Val Phe Pro Phe
332      515      520      525
334 Ser Asn Ile Arg Pro Gly Lys Arg Gln Thr Ser Val Ile Leu Ile Cys
335      530      535      540
337 Ile Trp Met Ala Gly Phe Leu Ile Ala Val Ile Pro Phe Trp Asn Lys
338 545      550      555      560
340 Asp Tyr Phe Gly Asn Phe Tyr Gly Lys Asn Gly Val Cys Phe Pro Leu

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date